

A. Harris

#15



ENTERED

1642

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/438,917

DATE: 02/25/2002 P.S.
TIME: 13:38:33

Input Set : A:\IU3446.txt

Output Set: N:\CRF3\02252002\I438917.raw

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4 <110> APPLICANT: Immusol Incorporated
5   Welch, Peter J.
6   Barber, Jack R.
8 <120> TITLE OF INVENTION: Tumor Suppressor Molecules and Methods
9   of Use
11 <130> FILE REFERENCE: 039316-0301
13 <140> CURRENT APPLICATION NUMBER: US 09/438,917
C--> 14 <141> CURRENT FILING DATE: 1999-11-11
16 <160> NUMBER OF SEQ ID NOS: 20
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 16
22 <212> TYPE: RNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: hairpin ribozyme
28 <400> SEQUENCE: 1
29 accuccccag aacccu                                     16
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 16
33 <212> TYPE: RNA
34 <213> ORGANISM: homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: misc_feature
38 <222> LOCATION: (1)...(16)
39 <223> OTHER INFORMATION: n = A,U,C or G
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44 <210> SEQ ID NO: 3
45 <211> LENGTH: 16
46 <212> TYPE: RNA
47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
51 <223> OTHER INFORMATION: hairpin ribozyme
53 <400> SEQUENCE: 3
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56 <210> SEQ ID NO: 4
57 <211> LENGTH: 16
58 <212> TYPE: RNA
59 <213> ORGANISM: homo sapiens
61 <220> FEATURE:
62 <221> NAME/KEY: misc_feature
63 <222> LOCATION: (1)...(16)

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64 <223> OTHER INFORMATION: n = A,U,C or G

66 <400> SEQUENCE: 4

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69 <210> SEQ ID NO: 5

70 <211> LENGTH: 1664

71 <212> TYPE: DNA

72 <213> ORGANISM: homo sapiens

74 <220> FEATURE:

75 <221> NAME/KEY: CDS

76 <222> LOCATION: (103)...(1525)

78 <400> SEQUENCE: 5

79 gcctgatgtc gtcccacgcc gtgccggctc tcaggcgccg gaagtgaagct gcgcacggcc 60

80 ggaagcggcg gacgcaggag gcctcgtgga ggacacagca gc atg gga cag tca 114

81 Met Gly Gln Ser

82 1

84 ggg agg tcc cgg cac cag aag cgc gcc ccg ccc cag gcg cag ctc cgc 162

85 Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln Ala Gln Leu Arg

86 5 10 15 20

88 aac ctc gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga 210

89 Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg

90 25 30 35

92 ggc tgc acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg 258

93 Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg

94 40 45 50

96 gtc atg gag ccc gtc act gcc agc cgt ctg cag gtt cgt aag aag aac 306

97 Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn

98 55 60 65

100 tcg ctg aag gac tgc gtg gca gtg gct ggg ccc ctc ggg gtc aca cac 354

101 Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His

102 70 75 80

104 ttt ctg atc cta gca aaa caa gag acc aat gtc tac ttt aag ctg atg 402

105 Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr Phe Lys Leu Met

106 85 90 95 100

108 cgc ctc cca gga ggc ccc acc ttg acc ttc cag gtc aag aag tac tcg 450

109 Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser

110 105 110 115

112 ctg gtg cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag 498

113 Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu

114 120 125 130

116 cag cag ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc 546

117 Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro

118 135 140 145

120 cat ggt atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc 594

121 His Gly Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe

122 150 155 160

124 ccc tcc atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc 642

125 Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys

126 165 170 175 180

128 ctc ctc atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac 690

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129	Leu	Leu	Ile	Asp	Tyr	Asn	Pro	Asp	Ser	Gln	Glu	Leu	Asp	Phe	Arg	His	
130					185					190					195		
132	tat	agc	atc	aaa	gtt	gtt	cct	gtg	ggc	gcg	agt	cgc	ggg	atg	aag	aag	738
133	Tyr	Ser	Ile	Lys	Val	Val	Pro	Val	Gly	Ala	Ser	Arg	Gly	Met	Lys	Lys	
134				200					205					210			
136	ctg	ctc	cag	gag	aag	ttc	ccc	aac	atg	agc	cgc	ctg	cag	gac	atc	agc	786
137	Leu	Leu	Gln	Glu	Lys	Phe	Pro	Asn	Met	Ser	Arg	Leu	Gln	Asp	Ile	Ser	
138			215				220						225				
140	gag	ctg	ctg	gcc	acg	ggc	gcg	ggg	ctg	tgc	gag	agc	gag	gca	gag	cct	834
141	Glu	Leu	Leu	Ala	Thr	Gly	Ala	Gly	Leu	Ser	Glu	Ser	Glu	Ala	Glu	Pro	
142		230					235						240				
144	gac	ggc	gac	cac	aac	atc	aca	gag	ctg	cct	cag	gct	gtc	gct	ggc	cgt	882
145	Asp	Gly	Asp	His	Asn	Ile	Thr	Glu	Leu	Pro	Gln	Ala	Val	Ala	Gly	Arg	
146	245				250					255						260	
148	ggc	aac	atg	cgg	gcc	cag	cag	agt	gca	gtg	cgg	ctc	acc	gag	atc	ggc	930
149	Gly	Asn	Met	Arg	Ala	Gln	Gln	Ser	Ala	Val	Arg	Leu	Thr	Glu	Ile	Gly	
150				265					270						275		
152	ccg	cgg	atg	aca	ctg	cag	ctc	atc	aag	gtc	cag	gag	ggc	gtc	ggg	gag	978
153	Pro	Arg	Met	Thr	Leu	Gln	Leu	Ile	Lys	Val	Gln	Glu	Gly	Val	Gly	Glu	
154			280						285					290			
156	ggc	aaa	gtg	atg	ttc	cac	agt	ttt	gtg	agc	aag	acg	gag	gag	gag	ctg	1026
157	Gly	Lys	Val	Met	Phe	His	Ser	Phe	Val	Ser	Lys	Thr	Glu	Glu	Glu	Leu	
158		295					300						305				
160	cag	gcc	atc	ctg	gaa	gcc	aag	gag	aag	aag	ctg	cgg	ctg	aag	gct	cag	1074
161	Gln	Ala	Ile	Leu	Glu	Ala	Lys	Glu	Lys	Lys	Leu	Arg	Leu	Lys	Ala	Gln	
162		310					315						320				
164	agg	cag	gcc	cag	cag	gcc	cag	aat	gtg	cag	cgc	aag	cag	gag	cag	cgg	1122
165	Arg	Gln	Ala	Gln	Gln	Ala	Gln	Asn	Val	Gln	Arg	Lys	Gln	Glu	Gln	Arg	
166	325				330					335						340	
168	gag	gcc	cac	aga	aag	aag	agc	ctg	gag	ggc	atg	aag	aag	gca	cgg	gtc	1170
169	Glu	Ala	His	Arg	Lys	Lys	Ser	Leu	Glu	Gly	Met	Lys	Lys	Ala	Arg	Val	
170				345						350					355		
172	ggg	ggt	agt	gat	gaa	gag	gcc	tct	ggg	atc	cct	tca	agg	acg	gcg	agc	1218
173	Gly	Gly	Ser	Asp	Glu	Glu	Ala	Ser	Gly	Ile	Pro	Ser	Arg	Thr	Ala	Ser	
174			360						365					370			
176	ctg	gag	ttg	ggt	gag	gac	gat	gat	gaa	cag	gaa	gat	gat	gac	atc	gag	1266
177	Leu	Glu	Leu	Gly	Glu	Asp	Asp	His	Glu	Gln	Glu	Asp	Asp	Asp	Ile	Glu	
178		375					380						385				
180	tat	ttc	tgc	cag	gcg	gtg	ggc	gag	gcg	ccc	agt	gag	gac	ctg	ttc	ccc	1314
181	Tyr	Phe	Cys	Gln	Ala	Val	Gly	Glu	Ala	Pro	Ser	Glu	Asp	Leu	Phe	Pro	
182		390					395						400				
184	gag	gcc	aag	cag	aaa	cgg	ctt	gcc	aag	tct	cca	ggg	cgg	aag	cgg	aag	1362
185	Glu	Ala	Lys	Gln	Lys	Arg	Leu	Ala	Lys	Ser	Pro	Gly	Arg	Lys	Arg	Lys	
186	405				410					415						420	
188	cgg	tgg	gaa	atg	gat	cga	ggc	agg	ggt	cgc	ctt	tgt	gac	cag	aag	ttt	1410
189	Arg	Trp	Glu	Met	Asp	Arg	Gly	Arg	Gly	Arg	Leu	Cys	Asp	Gln	Lys	Phe	
190				425					430						435		
192	ccc	aag	acc	aag	gac	aag	tcc	cag	gga	gcc	cag	gcc	agg	cgg	ggg	ccc	1458
193	Pro	Lys	Thr	Lys	Asp	Lys	Ser	Gln	Gly	Ala	Gln	Ala	Arg	Arg	Gly	Pro	

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194          440          445          450
196 aga ggg gct tcc cgg gat ggt ggg cga ggc cgg ggc cga ggc cgc cca      1506
197 Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro
198          455          460          465
200 ggg aag aga gtg gcc tga g cccaagccgc accggagcag cggctggatt      1555
201 Gly Lys Arg Val Ala *
202          470
204 gaacgccccca gattggggcc cgagatgtgg ccctcggttt cctttcataa aggagttgtg      1615
205 tccccagccc ttccactcca gtaaagaact gaattggcaa aaaaaaaaaa      1664
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 473
209 <212> TYPE: PRT
210 <213> ORGANISM: homo sapiens
212 <400> SEQUENCE: 6
213 Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln
214 1          5          10          15
215 Ala Gln Leu Arg Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe
216          20          25          30
217 Val Phe Thr Arg Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu
218          35          40          45
219 Asp Val Arg Arg Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val
220          50          55          60
221 Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu
222 65          70          75          80
223 Gly Val Thr His Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr
224          85          90          95
225 Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val
226          100          105          110
227 Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His
228          115          120          125
229 Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn
230          130          135          140
231 Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala Thr Met Phe
232 145          150          155          160
233 Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr
234          165          170          175
235 Ile Lys Arg Cys Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu
236          180          185          190
237 Asp Phe Arg His Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg
238          195          200          205
239 Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu
240          210          215          220
241 Gln Asp Ile Ser Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser
242 225          230          235          240
243 Glu Ala Glu Pro Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala
244          245          250          255
245 Val Ala Gly Arg Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu
246          260          265          270
247 Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu

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```

248          275          280          285
249 Gly Val Gly Glu Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr
250          290          295          300
251 Glu Glu Glu Leu Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg
252 305          310          315          320
253 Leu Lys Ala Gln Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys
254          325          330          335
255 Gln Glu Gln Arg Glu Ala His Arg Lys Ser Leu Glu Gly Met Lys
256          340          345          350
257 Lys Ala Arg Val Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser
258          355          360          365
259 Arg Thr Ala Ser Leu Glu Leu Gly Glu Asp Asp Asp Glu Gln Glu Asp
260          370          375          380
261 Asp Asp Ile Glu Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu
262 385          390          395          400
263 Asp Leu Phe Pro Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly
264          405          410          415
265 Arg Lys Arg Lys Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys
266          420          425          430
267 Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala
268          435          440          445
269 Arg Arg Gly Pro Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly
270          450          455          460
271 Arg Gly Arg Pro Gly Lys Arg Val Ala
272 465          470

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274 <210> SEQ ID NO: 7

275 <211> LENGTH: 87

276 <212> TYPE: DNA

277 <213> ORGANISM: Artificial Sequence

279 <220> FEATURE:

280 <223> OTHER INFORMATION: synthetic oligonucleotides

282 <221> NAME/KEY: misc_feature

283 <222> LOCATION: (1)...(87)

284 <223> OTHER INFORMATION: n = A,T,C or G

286 <400> SEQUENCE: 7

W--> 287 cgcgtaccag gtaatatacc acggaccgaa gtccgtgtgt ttctctggtn nnnttctnnn 60

W--> 288 nnnnnggatc ctgtttccgc ccggttt 87

290 <210> SEQ ID NO: 8

291 <211> LENGTH: 22

292 <212> TYPE: DNA

293 <213> ORGANISM: Artificial Sequence

295 <220> FEATURE:

296 <223> OTHER INFORMATION: synthetic oligonucleotide

298 <400> SEQUENCE: 8

299 gtccgtggtta tattacctgg ta 22

301 <210> SEQ ID NO: 9

302 <211> LENGTH: 20

303 <212> TYPE: DNA

304 <213> ORGANISM: Artificial Sequence

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\IU3446.txt

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20